

## WEST Search History





DATE: Thursday, November 03, 2005

<u>Hide?</u>	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
	<i>DB=PGPB,USPT,EPAB; PLUR=YES; OP=OR</i>		
<input type="checkbox"/>	L51	L50 and l17	2
<input type="checkbox"/>	L50	(424/179.1)![CCLS]	249
<input type="checkbox"/>	L49	L48 and l17	1
<input type="checkbox"/>	L48	(530/387.1,387.3,388.1,388.8)![CCLS]	5526
<input type="checkbox"/>	L47	6022966.pn.	1
<input type="checkbox"/>	L46	L45 and L44	1
<input type="checkbox"/>	L45	cancer\$ or tumor\$ or neoplas\$	175849
<input type="checkbox"/>	L44	5541287.pn.	1
<input type="checkbox"/>	L43	L42 and L36	88
<input type="checkbox"/>	L42	L41 or L40 or L38	267
<input type="checkbox"/>	L41	L37.clm.	245
<input type="checkbox"/>	L40	L37.ti.	12
<input type="checkbox"/>	L39	L37.ti	3560
<input type="checkbox"/>	L38	L37.ab.	31
<input type="checkbox"/>	L37	dota	3560
<input type="checkbox"/>	L36	L34 or L35	2631
<input type="checkbox"/>	L35	(534/10)![CCLS]	751
<input type="checkbox"/>	L34	(424/1.11  424/1.49  424/1.53  424/1.65  424/1.69)![CCLS]	2091
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<input type="checkbox"/>	L23	L21 and DOTA	57
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END OF SEARCH HISTORY

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2005, 15:19:05 ; Search time 120 Seconds  
(without alignments)  
702.615 Million cell updates/sec

Title: US-09-671-953B-5  
Perfect score: 1132  
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
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2	1118	98.8	218	4	AAB20359	Aab20359 Anti-chel
3	1113	98.3	218	4	AAB20360	Aab20360 Anti-chel
4	1079	95.3	218	8	ADQ98050	Adq98050 Chimeric
5	1078	95.2	218	8	ADQ98051	Adq98051 Chimeric
6	776	68.6	215	8	ADR23362	Adr23362 Human CD7
7	759	67.0	235	2	AAW82740	Aaw82740 Plasmid p
8	755.5	66.7	235	5	AAE27925	Aae27925 Human C2B
9	755.5	66.7	235	6	ABB82834	Abb82834 Antibody

10	755	66.7	213	8	ADL92471	Adl92471	Antibody
11	751	66.3	220	2	AAW07528	Aaw07528	Anti-HGF
12	750.5	66.3	235	3	AAB08025	Aab08025	A dimeric
13	749.5	66.2	234	5	AAO14066	Aao14066	Light cha
14	749.5	66.2	234	6	ABU08018	Abu08018	Human mon
15	749.5	66.2	234	7	ADF65776	Adf65776	Human mon
16	749.5	66.2	234	8	ADJ92516	Adj92516	Human SOJ
17	749	66.2	213	6	AAE34878	Aae34878	BIWA4/8 a
18	749	66.2	213	8	ADL15445	Adl15445	Humanised
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21	747	66.0	213	6	AAE34877	Aae34877	BIWA4 ant
22	747	66.0	213	8	ADL15441	Adl15441	Humanised
23	747	66.0	213	8	ADO00849	Ado00849	Humanised
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25	746	65.9	239	8	ADK70470	Adk70470	Respirato
26	745.5	65.9	240	6	ABJ38595	Abj38595	Hepatitis
27	744	65.7	215	8	ADQ31885	Adq31885	Antibody
28	742	65.5	215	8	ADQ16702	Adq16702	Modified
29	742	65.5	236	8	ADP79579	Adp79579	Chimeric
30	741.5	65.5	234	3	AA92239	Aay92239	Human bon
31	741	65.5	236	2	AA934096	Aay34096	Partial a
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34	740	65.4	233	3	AA93731	Aay93731	The kappa
35	740	65.4	233	6	AAE35886	Aae35886	Human 4.8
36	739.5	65.3	214	2	AA908599	Aay08599	Anti-huma
37	739	65.3	241	6	ABJ38593	Abj38593	Hepatitis
38	738.5	65.2	234	6	ABP55483	Abp55483	CJRA05 pr
39	738.5	65.2	240	6	ABJ38594	Abj38594	Hepatitis
40	738	65.2	235	2	AAW06180	Aaw06180	Humanised
41	737.5	65.2	214	8	ADH34591	Adh34591	023 light
42	737	65.1	213	2	AAW05830	Aaw05830	Humanised
43	737	65.1	215	6	ABR01469	Abr01469	Human ant
44	736.5	65.1	216	8	ADS87940	Ads87940	Anti-IFN-
45	736.5	65.1	216	8	ADS94937	Ads94937	Anti-IFN-

#### ALIGNMENTS

##### RESULT 1

AAB20358

ID AAB20358 standard; protein; 218 AA.

XX

AC AAB20358;

XX

DT 11-JUN-2001 (first entry)

XX

DE Anti-chelate antibody CHA255 light chain mutant N96C.

XX

KW Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;  
KW cancer; therapy; mutant; mutein.

XX

OS Mus musculus.

OS Synthetic.

XX

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PN	WO200122922-A2.	
XX		
PD	05-APR-2001.	
XX		
PF	27-SEP-2000; 2000WO-US026619.	
XX		
PR	27-SEP-1999; 99US-0156194P.	
PR	31-MAY-2000; 2000US-0208684P.	
XX		
PA	(REGC ) UNIV CALIFORNIA.	
XX		
PI	Meares C, Chmura A;	
XX		
DR	WPI; 2001-244971/25.	
DR	N-PSDB; AAF30633.	
XX		
PT	Nucleic acid encoding a mutant antibody comprising a reactive site that	
PT	specifically binds to a metal chelate useful as analytical agents and in	
PT	clinical diagnosis, as well as in the treatment of disease, particularly	
PT	cancer.	
XX		
PS	Disclosure; Fig 12; 100pp; English.	

XX  
 CC The invention provides a mutant antibody comprising a reactive site that  
 CC is not present in the wild-type of the antibody. The antibody also has a  
 CC complementarity determining region (CDR) that specifically binds to a  
 CC metal chelate against which the wild-type antibody is raised. The  
 CC reactive site of the mutant antibody is in a position proximate to or  
 CC within the CDR, such that the chelate and the antibody are able to form a  
 CC covalent bond. The present sequence is that of the light chain variable  
 CC region of anti-indium-EDTA monoclonal antibody CHA255, carrying an N96C  
 CC mutation. As an example of the method of the invention, rational computer  
 CC -aided design was used to develop an indium-EDTA chelate to covalently  
 CC bind to CHA255 in vivo. The premise was to allow the chelate to bind non-  
 CC covalently to CHA255 bound to a tumour and then to covalently attach the  
 CC chelate to the antibody, thereby trapping it at the tumour site. This  
 CC involved cloning the variable domains of CHA255 to construct a  
 CC human/mouse chimeric Fab fragment that could be expressed in Escherichia  
 CC coli, and the synthesis and screening of benzyl-EDTA chelates carrying  
 CC weakly electrophilic groups capable of conjugation of the antibody in  
 CC vivo. This Fab can be conjugated to a targeting moiety when desired. A  
 CC reactive site was incorporated into the antibody by engineering a Cys  
 CC residue at location Asn-96 or Ser-95 of the light chain, near the region  
 CC of the antibody to which the chelate bound. This was accomplished by site  
 CC -directed mutagenesis of a nucleic acid encoding the wild-type of the  
 CC anti-chelate antibody  
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 SQ Sequence 218 AA;

Query Match 99.8%; Score 1130; DB 4; Length 218;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-80;  
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RESULT 2  
 AAB20359  
 ID AAB20359 standard; protein; 218 AA.  
 XX  
 AC AAB20359;  
 XX  
 DT 11-JUN-2001 (first entry)  
 XX  
 DE Anti-chelate antibody CHA255 light chain.

XX  
 KW Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;  
 KW cancer; therapy.  
 XX  
 OS Mus musculus.  
 XX  
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 PN WO200122922-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 27-SEP-2000; 2000WO-US026619.  
 XX  
 PR 27-SEP-1999; 99US-0156194P.  
 PR 31-MAY-2000; 2000US-0208684P.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Meares C, Chmura A;  
 XX  
 DR WPI; 2001-244971/25.  
 DR N-PSDB; AAF30634.  
 XX  
 PT Nucleic acid encoding a mutant antibody comprising a reactive site that  
 PT specifically binds to a metal chelate useful as analytical agents and in

PT clinical diagnosis, as well as in the treatment of disease, particularly  
PT cancer.

XX

PS Disclosure; Fig 13; 100pp; English.

XX

CC The invention provides a mutant antibody comprising a reactive site that  
CC is not present in the wild-type of the antibody. The antibody also has a  
CC complementarity determining region (CDR) that specifically binds to a  
CC metal chelate against which the wild-type antibody is raised. The  
CC reactive site of the mutant antibody is in a position proximate to or  
CC within the CDR, such that the chelate and the antibody are able to form a  
CC covalent bond. The present sequence is that of the light chain of anti-  
CC indium-EDTA monoclonal antibody CHA255. As an example of the method of  
CC the invention, rational computer-aided design was used to develop an  
CC indium-EDTA chelate to covalently bind to CHA255 in vivo. The premise was  
CC to allow the chelate to bind non-covalently to CHA255 bound to a tumour  
CC and then to covalently attach the chelate to the antibody, thereby  
CC trapping it at the tumour site. This involved cloning the variable  
CC domains of CHA255 to construct a human/mouse chimeric Fab fragment that  
CC could be expressed in Escherichia coli, and the synthesis and screening  
CC of benzyl-EDTA chelates carrying weakly electrophilic groups capable of  
CC conjugation of the antibody in vivo. This Fab can be conjugated to a  
CC targeting moiety when desired. A reactive site was incorporated into the  
CC antibody by engineering a Cys residue at location Asn-96 or Ser-95 of the  
CC light chain, near the region of the antibody to which the chelate bound.  
CC This was accomplished by site-directed mutagenesis of a nucleic acid  
CC encoding the wild-type of the anti-chelate antibody

XX

SQ Sequence 218 AA;

Query Match 98.8%; Score 1118; DB 4; Length 218;

Best Local Similarity 99.5%; Pred. No. 6.4e-79;

Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy    121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
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Db    181 STLTLKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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RESULT 3

AAB20360

ID AAB20360 standard; protein; 218 AA.

XX

AC AAB20360;

XX



DT 11-JUN-2001 (first entry)  
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 DE Anti-chelate antibody CHA255 light chain mutant S95C.  
 XX  
 KW Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;  
 KW cancer; therapy; mutant; mutein.  
 XX  
 OS Mus musculus.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1. .23  
 FT /label= FR1  
 FT /note= "framework region 1"  
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 PN WO200122922-A2.  
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 PF 27-SEP-2000; 2000WO-US026619.  
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 PR 27-SEP-1999; 99US-0156194P.  
 PR 31-MAY-2000; 2000US-0208684P.  
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 PA (REGC ) UNIV CALIFORNIA.  
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 PI Meares C, Chmura A;

XX  
DR WPI; 2001-244971/25.  
DR N-PSDB; AAF30635.

XX  
PT Nucleic acid encoding a mutant antibody comprising a reactive site that  
PT specifically binds to a metal chelate useful as analytical agents and in  
PT clinical diagnosis, as well as in the treatment of disease, particularly  
PT cancer.

XX  
PS Disclosure; Fig 14; 100pp; English.

The invention provides a mutant antibody comprising a reactive site that is not present in the wild-type of the antibody. The antibody also has a complementarity determining region (CDR) that specifically binds to a metal chelate against which the wild-type antibody is raised. The reactive site of the mutant antibody is in a position proximate to or within the CDR, such that the chelate and the antibody are able to form a covalent bond. The present sequence is that of the light chain variable region of anti-indium-EDTA monoclonal antibody CHA255, carrying a S95C mutation. As an example of the method of the invention, rational computer-aided design was used to develop an indium-EDTA chelate to covalently bind to CHA255 in vivo. The premise was to allow the chelate to bind non-covalently to CHA255 bound to a tumour and then to covalently attach the chelate to the antibody, thereby trapping it at the tumour site. This involved cloning the variable domains of CHA255 to construct a human/mouse chimeric Fab fragment that could be expressed in *Escherichia coli*, and the synthesis and screening of benzyl-EDTA chelates carrying weakly electrophilic groups capable of conjugation of the antibody in vivo. This Fab can be conjugated to a targeting moiety when desired. A reactive site was incorporated into the antibody by engineering a Cys residue at location Asn-96 or Ser-95 of the light chain, near the region of the antibody to which the chelate bound. This was accomplished by site-directed mutagenesis of a nucleic acid encoding the wild-type of the anti-chelate antibody

XX  
SQ Sequence 218 AA;

Query Match 98.3%; Score 1113; DB 4; Length 218;  
Best Local Similarity 99.1%; Pred. No. 1.6e-78;  
Matches 216; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180

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QY 181 STLTLKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218

Db 181 STLTLKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218

RESULT 4

ADQ98050

ID ADQ98050 standard; protein; 218 AA.

XX

AC ADQ98050;

XX

DT 21-OCT-2004 (first entry)

XX

DE Chimeric murine 2D12.5 variable light chain fused to human TTCL protein.

XX

KW murine; mouse; chimeric; human; TTCL; tetanus toxin;

KW magnetic resonance imaging; lanthanide luminescence; gamma-emissions;

KW single photon emission tomography; SPET; cancer; cytostatic;

KW immunosuppressive; multi-functional antibody; metal chelate;

KW antigen recognition domain; in vivo imaging;

KW cell-antibody-metal chelate complex; emission tomography.

XX

OS Mus musculus.

OS Homo sapiens.

OS Chimeric.

XX

PN WO2004065569-A2.

XX

PD 05-AUG-2004.

XX

PF 23-JAN-2004; 2004WO-US001808.

XX

PR 23-JAN-2003; 2003US-00350555.

PR 22-JUL-2003; 2003US-00625047.

PR 31-JUL-2003; 2003US-00631258.

XX

PA (REGC ) UNIV CALIFORNIA.

XX

PI Meares C, Corneillie T;

XX

DR WPI; 2004-580725/56.

DR N-PSDB; ADQ98054.

XX

PT Novel mutant antibody comprising reactive site not present in wild-type

PT of antibody and antigen recognition domain that recognizes macrocyclic

PT metal chelate having four nitrogen atoms, useful for treating cancer or

PT autoimmune diseases.

XX

PS Claim 41; SEQ ID NO 27; 208pp; English.

XX

CC This invention relates to multi-functional antibodies that recognise

CC chelating agents and metal chelates, particularly macrocyclic metal

CC chelates. Specifically, it refers to an antibody that comprises a metal

CC chelate bound to an antigen recognition domain, where the metal chelate

CC has a reactive functional group of complementary reactivity to the

CC reactive site of the antibody. This reactive site is the side chain of a

CC naturally occurring amino acid e.g. the -SH group side chain of a

CC cysteine residue (not present in the wild type) which can be used to form

CC a covalent bond between the reactive site of the antibody and the

CC reactive functional group of the metal chelate. The present invention

CC describes using these antibodies for in vivo imaging where the antibody



FH Key Location/Qualifiers  
 FT Misc-difference 55  
 FT /note= "Wild type Asn substituted for Cys"  
 XX  
 PN WO2004065569-A2.  
 XX  
 PD 05-AUG-2004.  
 XX  
 PF 23-JAN-2004; 2004WO-US001808.  
 XX  
 PR 23-JAN-2003; 2003US-00350555.  
 PR 22-JUL-2003; 2003US-00625047.  
 PR 31-JUL-2003; 2003US-00631258.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Meares C, Corneillie T;  
 XX  
 DR WPI; 2004-580725/56.  
 DR N-PSDB; ADQ98055.  
 XX  
 PT Novel mutant antibody comprising reactive site not present in wild-type  
 PT of antibody and antigen recognition domain that recognizes macrocyclic  
 PT metal chelate having four nitrogen atoms, useful for treating cancer or  
 PT autoimmune diseases.  
 XX  
 PS Claim 41; SEQ ID NO 28; 208pp; English.  
 XX  
 CC This invention relates to multi-functional antibodies that recognise  
 CC chelating agents and metal chelates, particularly macrocyclic metal  
 CC chelates. Specifically, it refers to an antibody that comprises a metal  
 CC chelate bound to an antigen recognition domain, where the metal chelate  
 CC has a reactive functional group of complementary reactivity to the  
 CC reactive site of the antibody. This reactive site is the side chain of a  
 CC naturally occurring amino acid e.g. the -SH group side chain of a  
 CC cysteine residue (not present in the wild type) which can be used to form  
 CC a covalent bond between the reactive site of the antibody and the  
 CC reactive functional group of the metal chelate. The present invention  
 CC describes using these antibodies for in vivo imaging where the antibody  
 CC comprises a targeting moiety that binds specifically to a cell via a cell  
 CC surface receptor or antigen thus forming a cell-mutant antibody complex.  
 CC On addition of the metal chelate, a cell-antibody-metal chelate complex  
 CC is formed that can be detected using emission tomography, magnetic  
 CC resonance imaging, lanthanide luminescence, gamma-emissions or single  
 CC photon emission tomography (SPET). As such, this method is useful for  
 CC treating a subject with cancer and pharmaceutical compositions exhibit  
 CC cytostatic and immunosuppressive activities. This polypeptide sequence is  
 CC the chimeric mutant N53C murine antibody 2D12.5 variable light chain  
 CC protein fused to the human anti-tetanus toxin antibody kappa light chain  
 CC constant region of the invention.  
 XX  
 SQ Sequence 218 AA;

Query Match 95.2%; Score 1078; DB 8; Length 218;  
 Best Local Similarity 95.9%; Pred. No. 8.2e-76;  
 Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60  
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 Db 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120

Qy 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180  
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 Db 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180

Qy 181 STLTLKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218  
 |||  
 Db 181 STLTLKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218

RESULT 6

ADR23362

ID ADR23362 standard; protein; 215 AA.

XX

AC ADR23362;

XX

DT 04-NOV-2004 (first entry)

XX

DE Human CD72-targeted IgG1 light chain.

XX

KW Human; CD72; B-lymphocyte; receptor; scFv; antibody; cytostatic;  
 KW immunosuppressive; cancer; autoimmune disease; gene therapy.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Region	1. .109
----	--------	---------

FT		/label= V_region
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FT	Region	110. .215
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FT		/label= C_region
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XX

PN WO2004067569-A1.

XX

PD 12-AUG-2004.

XX

PF 27-JAN-2003; 2003WO-EP050004.

XX

PR 27-JAN-2003; 2003WO-EP050004.

XX

PA (CRUC-) CRUCCELL HOLLAND BV.

XX

PI Bakker ABH, Marissen WE;

XX

DR WPI; 2004-580978/56.

DR N-PSDB; ADR23361.

XX

PT New internalizing human binding molecules capable of specifically binding  
 PT to CD72, useful for diagnosing and/or treating B-cell associated  
 PT diseases, such as cancer or autoimmune disorders.

XX

PS Example 5; SEQ ID NO 54; 174pp; English.

XX

CC The present sequence is the protein sequence of the light chain of human  
CC IgG1 antibody 025, which specifically recognises human B cell associated  
CC antigen CD72. An scFv ADR23324 selected from an antibody phage display  
CC library was shown to specifically recognise the human CD72 receptor. The  
CC scFv was recloned in IgG expression vector C01 using primers designed to  
CC restore complete human frameworks, thereby generating antibody 025. Such  
CC anti-CD72 immunoglobulins or their antigen-binding fragments can be used  
CC as internalising human binding molecules of the invention. These  
CC internalising human binding molecules are capable of (specifically)  
CC binding to CD72 or its antigenic determinant, and preferably bind to CD72  
CC associated with cells. Upon binding to CD72 present on the surface of  
CC target cells, the binding molecules internalise. In addition to the  
CC internalising human binding molecules, the invention provides  
CC immunoconjugates comprising an internalising human binding molecule and a  
CC tag (toxic substance, radioactive substance, liposome and/or enzyme),  
CC nucleic acids encoding these, and compositions comprising them. The  
CC internalising human binding molecule, immunoconjugate, nucleic acid  
CC molecule or composition can be used in the diagnosis and/or treatment of  
CC a B cell associated disorder or disease, especially a B cell associated  
CC cancer and B cell associated autoimmune disorder (claimed).

XX

SQ Sequence 215 AA;

Query Match 68.6%; Score 776; DB 8; Length 215;  
Best Local Similarity 73.5%; Pred. No. 2.4e-52;  
Matches 161; Conservative 16; Mismatches 36; Indels 6; Gaps 3;

Qy 2 SAVVTQESALTTSPGETVTLTCSRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV 61  
|: :||: |: : |:| :||: | | ||: |:| :| | || |:|  
Db 1 SSELTDQDPAVSVALGQTVRITCQ---GDSLRSYYASWYQQKPGQAPVPLVIYGKNNRPSGI 57

Qy 62 PARFSGSLIGDKAALTITGAQTEDEARYFCALWYSC--LWVFGGGTKLTVLSRTVAAPSV 119  
| |||| |: |:||||| ||| |:| | ||||| |||||  
Db 58 PDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLG-TVAAPSV 116

Qy 120 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179  
|||||  
Db 117 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 176

Qy 180 SSTLTLSKADYEEKHKVYACEVTHQGLSXPVTKSFNRGEC 218  
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Db 177 SSTLTLSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC 215

us-09-671-953b-5.ra1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2005, 15:23:21 ; Search time 30 Seconds  
(without alignments)  
542.450 Million cell updates/sec

Title: US-09-671-953B-5  
Perfect score: 1132  
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	759	67.0	235	3	US-09-423-439-18	Sequence 18, Appl
2	751	66.3	220	3	US-08-952-235-1	Sequence 1, Appli
3	751	66.3	220	4	US-09-669-971-1	Sequence 1, Appli
4	740	65.4	233	4	US-09-472-087-15	Sequence 15, Appl
5	740	65.4	233	4	US-09-472-087-67	Sequence 67, Appl
6	738	65.2	235	4	US-09-011-769A-27	Sequence 27, Appl
7	735	64.9	213	3	US-08-397-411-12	Sequence 12, Appl
8	734.5	64.9	491	4	US-10-011-125A-2	Sequence 2, Appli
9	734	64.8	236	4	US-09-315-926A-79	Sequence 79, Appl
10	732	64.7	235	4	US-09-472-087-14	Sequence 14, Appl
11	732	64.7	235	4	US-09-472-087-65	Sequence 65, Appl
12	730.5	64.5	214	4	US-09-472-087-71	Sequence 71, Appl
13	730.5	64.5	224	4	US-09-456-090A-84	Sequence 84, Appl
14	730.5	64.5	224	4	US-09-453-234-84	Sequence 84, Appl
15	729.5	64.4	234	4	US-09-472-087-17	Sequence 17, Appl
16	729.5	64.4	234	4	US-09-472-087-69	Sequence 69, Appl
17	728.5	64.4	224	4	US-09-456-090A-46	Sequence 46, Appl



					us-09-671-953b-5.ra		
18	728.5	64.4	224	4	US-09-453-234-46	Sequence	46, Appl
19	728.5	64.4	234	4	US-09-740-002-24	Sequence	24, Appl
20	728	64.3	214	1	US-08-458-516-12	Sequence	12, Appl
21	727	64.2	233	3	US-09-485-737B-69	Sequence	69, Appl
22	727	64.2	233	4	US-10-071-485-69	Sequence	69, Appl
23	726	64.1	235	3	US-09-171-945-17	Sequence	17, Appl
24	725.5	64.1	224	4	US-09-456-090A-36	Sequence	36, Appl
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27	725.5	64.1	226	4	US-09-453-234-74	Sequence	74, Appl
28	724.5	64.0	214	3	US-09-247-352-4	Sequence	4, Appli
29	724.5	64.0	214	4	US-09-466-635-4	Sequence	4, Appli
30	723.5	63.9	213	3	US-08-630-820-6	Sequence	6, Appli
31	723.5	63.9	213	4	US-09-273-453-6	Sequence	6, Appli
32	723.5	63.9	236	1	US-08-157-101A-5	Sequence	5, Appli
33	723	63.9	219	3	US-09-027-449-72	Sequence	72, Appl
34	723	63.9	219	3	US-09-026-985-72	Sequence	72, Appl
35	723	63.9	219	4	US-09-121-952A-72	Sequence	72, Appl
36	723	63.9	219	4	US-09-234-340A-72	Sequence	72, Appl
37	723	63.9	239	4	US-09-627-896B-22	Sequence	22, Appl
38	723	63.9	242	3	US-09-027-449-56	Sequence	56, Appl
39	723	63.9	242	3	US-08-804-444A-56	Sequence	56, Appl
40	723	63.9	242	3	US-09-026-985-56	Sequence	56, Appl
41	723	63.9	242	4	US-09-121-952A-56	Sequence	56, Appl
42	723	63.9	242	4	US-09-234-340A-56	Sequence	56, Appl
43	722.5	63.8	214	3	US-08-397-411-5	Sequence	5, Appli
44	722	63.8	214	2	US-07-934-373C-24	Sequence	24, Appl
45	722	63.8	214	3	US-08-437-642B-24	Sequence	24, Appl

# ALIGNMENTS

## RESULT 1

US-09-423-439-18

; Sequence 18, Application US/09423439  
; Patent No. 6339070

### GENERAL INFORMATION:

APPLICANT: EMERY, Stephen Charles

BLAKEY, David Charles

TITLE OF INVENTION: CHEMICAL COMPOUNDS

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Winthrop, L.L.P.

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/423,439

FILING DATE: 09-No. 6339070-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB98/01294

FILING DATE: 05-MAY-1998

APPLICATION NUMBER: GB 9709421.3

FILING DATE: 10-MAY-1997

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us-09-671-953b-5.ra
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 235 amino acids
:   TYPE: amino acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-423-439-18

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Query Match          67.0%; Score 759; DB 3; Length 235;
Best Local Similarity 72.2%; Pred. No. 1.6e-67;
Matches 156; Conservative 15; Mismatches 39; Indels 6; Gaps 3;

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Qy      4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
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Db      81 ARFSGSGSGTSYSLTISRVEAEDAATYYCQHWSSKPPTFGGGTKLEI-KRTVAAPSVFIF 139

Qy      123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSST 182
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Db      140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSST 199

Qy      183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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us-09-671-953b-5.rapb

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2005, 15:34:17 ; Search time 113.5 Seconds  
(without alignments)  
802.937 Million cell updates/sec

Title: US-09-671-953B-5  
Perfect score: 1132  
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Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

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Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1079	95.3	218	16	US-10-625-047-27	Sequence 27, Appl

				us-09-671-953b-5.rapb		
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3	1079	95.3	218	18	US-10-350-555-27	Sequence 27, Appl
4	1078	95.2	218	16	US-10-625-047-28	Sequence 28, Appl
5	1078	95.2	218	17	US-10-631-258-28	Sequence 28, Appl
6	1078	95.2	218	18	US-10-350-555-28	Sequence 28, Appl
7	755.5	66.7	235	16	US-10-723-003-42	Sequence 42, Appl
8	755.5	66.7	235	20	US-11-004-639-42	Sequence 42, Appl
9	755	66.7	213	17	US-10-822-231-3	Sequence 3, Appli
10	755	66.7	213	18	US-10-880-028-49	Sequence 49, Appl
11	755	66.7	213	18	US-10-880-320-49	Sequence 49, Appl
12	751	66.3	220	9	US-09-995-693-1	Sequence 1, Appli
13	751	66.3	220	14	US-10-232-408-1	Sequence 1, Appli
14	750.5	66.3	235	20	US-11-019-180-2	Sequence 2, Appli
15	749.5	66.2	234	10	US-09-848-832-4	Sequence 4, Appli
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17	749.5	66.2	234	15	US-10-461-148-2	Sequence 2, Appli
18	749	66.2	213	14	US-10-150-475A-8	Sequence 8, Appli
19	749	66.2	213	16	US-10-704-522-8	Sequence 8, Appli
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26	746	65.9	215	17	US-10-724-274-32	Sequence 32, Appl
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28	744	65.7	215	17	US-10-818-068-26	Sequence 26, Appl
29	744	65.7	215	17	US-10-822-300-141	Sequence 141, App
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34	742	65.5	239	16	US-10-737-290-142	Sequence 142, App
35	741	65.5	213	15	US-10-435-299-12	Sequence 12, Appl
36	741	65.5	213	17	US-10-822-300-135	Sequence 135, App
37	741	65.5	215	18	US-10-916-758-16	Sequence 16, Appl
38	740.5	65.4	236	17	US-10-961-567A-6	Sequence 6, Appli
39	740	65.4	233	14	US-10-153-382-11	Sequence 11, Appl
40	740	65.4	233	16	US-10-612-497-15	Sequence 15, Appl
41	740	65.4	233	16	US-10-612-497-67	Sequence 67, Appl
42	740	65.4	233	16	US-10-776-649-15	Sequence 15, Appl
43	740	65.4	233	16	US-10-776-649-67	Sequence 67, Appl
44	740	65.4	233	20	US-11-085-368-11	Sequence 11, Appl
45	740	65.4	233	20	US-11-085-368-47	Sequence 47, Appl

#### ALIGNMENTS

RESULT 1  
 US-10-625-047-27  
 ; Sequence 27, Application US/10625047  
 ; Publication No. US20040198962A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Meares, Claude  
 ; APPLICANT: Corneillie, Todd  
 ; APPLICANT: The Regents of the University of California  
 ; TITLE OF INVENTION: Multi-Functional Antibodies  
 ; FILE REFERENCE: 023070-130910US  
 ; CURRENT APPLICATION NUMBER: US/10/625,047  
 ; CURRENT FILING DATE: 2003-07-22  
 ; PRIOR APPLICATION NUMBER: US 10/350,555  
 ; PRIOR FILING DATE: 2003-01-23

us-09-671-953b-5.rapb

; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:native cloned  
; OTHER INFORMATION: chimeric murine 2D12.5 light chain variable region  
; OTHER INFORMATION: (VL) fused to human anti-tetanus toxin antibody  
; OTHER INFORMATION: kappa light chain constant region (TTCL)  
US-10-625-047-27

Query Match 95.3%; Score 1079; DB 16; Length 218;  
Best Local Similarity 95.9%; Pred. No. 2.1e-83;  
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy	1	RSVVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG	60
Db	1	RSVVVTQESALTTSPGETVTLTCRSSSTGAVTTSNYANWVQEKPDHLFTGLIGGNNRPPG	60
Qy	61	VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF	120
Db	61	VPARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTKLTVLSRTVAAPSVF	120
Qy	121	IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS	180
Db	121	IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS	180
Qy	181	STLTLSKADYEEKHKVYACEVTHQGLSXPVTKSFNRGEC	218
Db	181	STLTLSKADYEEKHKVYACEVTHQGLSLPVTKSFNRGEC	218

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2005, 15:22:51 ; Search time 25.5 Seconds  
(without alignments)  
822.559 Million cell updates/sec

Title: US-09-671-953B-5  
Perfect score: 1132  
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pirl:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	740	65.4	215	2	JE0242	Ig kappa chain NIG
2	729	64.4	215	2	JE0244	Ig kappa chain NIG
3	724.5	64.0	214	2	PC4156	Ig lambda chain V
4	716	63.3	215	2	JE0243	Ig kappa chain NIG
5	682.5	60.3	216	2	JE0241	Ig kappa chain Am3
6	675	59.6	215	2	A23746	Ig kappa chain V-I
7	578.5	51.1	135	2	S52059	JC-kappa protein -
8	552.5	48.8	240	2	S06084	Ig kappa chain pre
9	544	48.1	106	1	K3HU	Ig kappa chain C r
10	543.5	48.0	287	4	PC4402	pelB leader/Ig hea
11	537	47.4	128	2	S52450	Ig lambda chain V
12	530.5	46.9	220	2	A31790	Ig kappa chain V r
13	529	46.7	129	1	L1MS4E	Ig lambda-1 chain

14	522	46.1	235	2	S25058	Ig kappa chain - m
15	521	46.0	113	2	S06819	Ig lambda chain V
16	519.5	45.9	112	2	S06818	Ig lambda chain V
17	517	45.7	106	2	S20654	Ig lambda chain V
18	515	45.5	219	2	S38865	Ig kappa chain - m
19	514	45.4	225	2	S37484	Ig kappa chain - m
20	509.5	45.0	114	2	S06820	Ig lambda chain V
21	509.5	45.0	234	2	S14237	Ig kappa chain pre
22	509	45.0	99	2	A37927	Ig kappa chain C r
23	506.5	44.7	230	2	S33161	Ig kappa chain - s
24	503.5	44.5	218	2	S68241	Ig kappa chain V r
25	503	44.4	99	2	S26653	Ig kappa chain C r
26	501.5	44.3	214	2	S68212	Ig kappa chain (Ma
27	499.5	44.1	225	2	JL0029	Ig kappa chain pre
28	498.5	44.0	218	2	JC5810	monoclonal antibod
29	497.5	43.9	234	2	S01320	Ig kappa chain pre
30	495.5	43.8	114	2	S06822	Ig lambda chain V
31	495	43.7	113	2	B54256	Ig lambda-1 chain
32	492	43.5	217	2	S42772	Ig kappa chain - m
33	492	43.5	219	2	S16112	Ig kappa chain V r
34	491	43.4	129	1	L2MS35	Ig lambda-2 chain
35	488.5	43.2	219	2	PC4203	Ig kappa chain (mo
36	485	42.8	235	2	S25749	Ig lambda chain -
37	484.5	42.8	99	2	PH1089	Ig lambda chain V
38	482	42.6	99	2	S14582	Ig lambda chain V
39	482	42.6	113	2	S06821	Ig lambda chain V
40	482	42.6	219	2	S52028	Ig kappa chain - m
41	477	42.1	97	2	PH1090	Ig lambda chain V
42	477	42.1	116	1	L1MSV	Ig lambda-1 chain
43	475.5	42.0	210	2	A56169	Ig kappa chain V r
44	472	41.7	99	2	S14584	Ig lambda chain V
45	469	41.4	100	2	PH1088	Ig lambda chain V

#### ALIGNMENTS

##### RESULT 1

JE0242

Ig kappa chain NIG26 precursor - human

C;Species: Homo sapiens (man)

C;Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

C;Accession: JE0242

R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.

submitted to JIPID, November 1998

A;Description: Structure relationship of kappatype light chains with AL amyloidosis: Multiple deletions found in a VkIV protein.

A;Reference number: JE0241

A;Accession: JE0242

A;Molecule type: protein

A;Residues: 1-215 <ALI>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 65.4%; Score 740; DB 2; Length 215;  
Best Local Similarity 70.4%; Pred. No. 7.9e-49;

Matches 152; Conservative 17; Mismatches 43; Indels 4; Gaps 3;

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Qy      4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
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Db      3 VLTQSPGTLSSLSPGERATLSCRAS--QSVSNYYLAWYQQKPGQAPSLLIYDASSRATGIP 60

Qy     63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
      ||||  |  ||:| : || | |:|  :  | ||  ||: :  ||| |||||
Db     61 DRFSGSGSGTDFILTISGLEPEDFAVYYCQQYDRPPWTFGQGTKVEI-KRTVAAPSVFIF 119

Qy    123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSST 182
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSST 179

Qy    183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    180 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
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us-09-671-953b-5.rup

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2005, 15:22:03 ; Search time 116.5 Seconds  
(without alignments)  
958.225 Million cell updates/sec

Title: US-09-671-953B-5  
Perfect score: 1132  
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	734	64.8	235	2	Q6PJF2	Q6pjf2 homo sapien
2	733	64.8	235	2	Q6GMW0	Q6gmw0 homo sapien
3	732	64.7	236	2	Q6GMW1	Q6gmw1 homo sapien
4	727.5	64.3	236	2	Q7Z3Y4	Q7z3y4 homo sapien
5	727	64.2	234	2	Q7Z473	Q7z473 homo sapien
6	723.5	63.9	236	2	Q6PIH7	Q6pih7 homo sapien
7	722.5	63.8	236	2	Q6GMX9	Q6gmx9 homo sapien
8	721.5	63.7	236	2	Q6P5S8	Q6p5s8 homo sapien
9	721	63.7	235	2	Q6GMV9	Q6gmv9 homo sapien
10	720.5	63.6	236	2	Q6GMX0	Q6gmx0 homo sapien
11	717.5	63.4	236	2	Q6PIL8	Q6pil8 homo sapien
12	715.5	63.2	236	2	Q6GMX8	Q6gmx8 homo sapien
13	704	62.2	236	2	Q6PIT5	Q6pit5 homo sapien
14	702.5	62.1	236	2	Q6PIH4	Q6pih4 homo sapien
15	697	61.6	239	2	Q8TCD0	Q8tcd0 homo sapien
16	696	61.5	240	2	Q6PIH6	Q6pih6 homo sapien
17	694	61.3	239	2	Q8NEK0	Q8nek0 homo sapien
18	666	58.8	239	2	Q6P491	Q6p491 homo sapien
19	564.5	49.9	120	2	Q6P5R5	Q6p5r5 homo sapien
20	544	48.1	106	1	KAC_HUMAN	P01834 homo sapien
21	535	47.3	129	1	LV1E_MOUSE	P01727 mus musculu

					us-09-671-953b-5.rup			
22	530	46.8	129	1	LV1D_MOUSE	P01726	mus	musculu
23	529	46.7	129	1	LV1B_MOUSE	P01724	mus	musculu
24	523	46.2	129	2	Q8VDE2	Q8vde2	mus	musculu
25	522.5	46.2	238	2	Q66JS7	Q66js7	mus	musculu
26	521	46.0	110	1	LV1C_MOUSE	P01725	mus	musculu
27	514.5	45.5	113	2	Q8CGS1	Q8cgs1	mus	musculu
28	510.5	45.1	236	2	Q7TS98	Q7ts98	mus	musculu
29	507.5	44.8	109	2	Q9ET13	Q9et13	mus	musculu
30	502	44.3	219	2	Q65ZC0	Q65zc0	mus	musculu
31	497.5	43.9	241	2	Q63ZX4	Q63zx4	mus	musculu
32	491	43.4	129	1	LV2B_MOUSE	P01729	mus	musculu
33	477	42.1	117	1	LV1A_MOUSE	P01723	mus	musculu
34	454	40.1	117	1	LV2A_MOUSE	P01728	mus	musculu
35	442.5	39.1	236	2	Q8NEJ1	Q8nej1	homo	sapien
36	440	38.9	235	2	Q6IN99	Q6in99	homo	sapien
37	435	38.4	248	2	Q7SYU1	Q7syu1	xenopus	lae
38	432	38.2	233	2	Q8TBC9	Q8tbc9	homo	sapien
39	430.5	38.0	230	2	Q7Z2U3	Q7z2u3	homo	sapien
40	430.5	38.0	236	2	Q6PIQ7	Q6piq7	homo	sapien
41	428.5	37.9	236	2	Q6GMV7	Q6gmv7	homo	sapien
42	428.5	37.9	236	2	Q6IPQ0	Q6ipq0	homo	sapien
43	427.5	37.8	234	2	Q7Z2U7	Q7z2u7	homo	sapien
44	426.5	37.7	236	2	Q6GMX4	Q6gmx4	homo	sapien
45	426	37.6	231	2	Q6GNB8	Q6gnb8	xenopus	lae

#### ALIGNMENTS

#### RESULT 1

Q6PJF2

ID Q6PJF2 PRELIMINARY; PRT; 235 AA.  
AC Q6PJF2;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human

```

us-09-671-953b-5.rup
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC016380; AAH16380.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

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Query Match 64.8%; Score 734; DB 2; Length 235;  
Best Local Similarity 70.4%; Pred. No. 1.5e-56;  
Matches 152; Conservative 18; Mismatches 42; Indels 4; Gaps 3;

Best Local Similarity 70.4%; Pred. No. 1.5e-56;

Matches 152; Conservative 18; Mismatches 42; Indels 4; Gaps 3;

Qy	4	VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP	62
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Qy	63	ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF	122
Db	81	DRFSGSGSGTDFTLTISRLEPEDFAVYYCQYQGSSQGTFGPGTKVDI-KRTVAAPSVFIF	139
Qy	123	PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSST	182
Db	140	PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSST	199
Qy	183	LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC	218
Db	200	LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	235

Db 23 VLTQSPATLSLSPGERATLSCRAS--QIVSSAYLAWYQQKPGQAPRLLMFGSSSRATGIP 80

Qy 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122

Db 81 DRFSGSGSGTDFLTISRLEPEDFAVYYCQQYGSSQGTFGPGTKVDI-KRTVAAPSVFIF 139

Qy 123 PPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSST 182

Db 140 PPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSST 199

QY 183 LTLSKADYEKHKVYACEVTHQGLSXPTKSFNRGEC 218

Db 200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNREGC 235

OM protein - protein search, using sw model

Result	Score	Query Match	Length	DB	ID	Description
1	1132	99.8	218	4	AAB20360	Aab20360 Anti-chel
2	1122	98.9	218	4	AAB20359	Aab20359 Anti-chel
3	1113	98.1	218	4	AAB20358	Aab20358 Anti-chel
4	1083	95.5	218	8	ADQ98050	Adq98050 Chimeric
5	1082	95.4	218	8	ADQ98051	Adq98051 Chimeric
6	779	68.7	215	8	ADR23362	Adr23362 Human CD7
7	759.5	67.0	235	5	AAE27925	Aae27925 Human C2B
8	759.5	67.0	235	6	ABB82834	Abb82834 Antibody
9	759	66.9	213	8	ADL92471	Adl92471 Antibody

10	757	66.8	235	2	AAW82740	Aaw82740	Plasmid p
11	754.5	66.5	235	3	AAB08025	Aab08025	A dimeric
12	753	66.4	213	6	AAE34878	Aae34878	BIWA4/8 a
13	753	66.4	213	8	ADL15445	Adl15445	Humanised
14	753	66.4	213	8	ADO00853	Ado00853	Humanised
15	751	66.2	213	6	AAE35326	Aae35326	Humanised
16	751	66.2	213	6	AAE34877	Aae34877	BIWA4 ant
17	751	66.2	213	8	ADL15441	Adl15441	Humanised
18	751	66.2	213	8	ADO00849	Ado00849	Humanised
19	751	66.2	236	8	ADP79579	Adp79579	Chimeric
20	750	66.1	220	2	AAW07528	Aaw07528	Anti-HGF
21	746	65.8	215	8	ADQ31891	Adq31891	Antibody
22	744	65.6	215	8	ADQ31885	Adq31885	Antibody
23	743.5	65.6	234	5	AAO14066	Aao14066	Light cha
24	743.5	65.6	234	6	ABU08018	Abu08018	Human mon
25	743.5	65.6	234	7	ADF65776	Adf65776	Human mon
26	743.5	65.6	234	8	ADJ92516	Adj92516	Human SOJ
27	743	65.5	233	3	AA93704	Aay93704	The kappa
28	743	65.5	233	3	AA93731	Aay93731	The kappa
29	743	65.5	233	6	AAE35886	Aae35886	Human 4.8
30	743	65.5	239	8	ADK70470	Adk70470	Respirato
31	741.5	65.4	240	6	ABJ38595	Abj38595	Hepatitis
32	741	65.3	213	2	AAW05830	Aaw05830	Humanised
33	740.5	65.3	234	3	AA92239	Aay92239	Human bon
34	739.5	65.2	234	6	ABP55483	Abp55483	CJRA05 pr
35	739	65.2	215	8	ADQ16702	Adq16702	Modified
36	738	65.1	213	6	AAE33521	Aae33521	Human AQC
37	738	65.1	232	8	ADP79583	Adp79583	2H7.v16 L
38	736	64.9	235	2	AAW06180	Aaw06180	Humanised
39	736	64.9	236	2	AA934096	Aay34096	Partial a
40	735.5	64.9	214	8	ADH34591	Adh34591	023 light
41	735.5	64.9	349	2	AAR12128	Aar12128	1B1 IgG a
42	735.5	64.9	414	2	AAR13111	Aar13111	1B1 IgG a
43	735.5	64.9	414	2	AAR13018	Aar13018	1B1 IgG a
44	735	64.8	213	4	AAB83157	Aab83157	Gangliosi
45	735	64.8	215	6	ABR01469	Abr01469	Human ant

#### ALIGNMENTS

##### RESULT 1

AAB20360

ID AAB20360 standard; protein; 218 AA.

XX

AC AAB20360;

XX

DT 11-JUN-2001 (first entry)

XX

DE Anti-chelate antibody CHA255 light chain mutant S95C.

XX

KW Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;

KW cancer; therapy; mutant; mutein.

XX

OS Mus musculus.

OS Synthetic.

XX

FH	Key	Location/Qualifiers
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FT		/note= "framework region 1"
FT	Region	24. .37
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FT	Region	38. .52
FT		/label= FR2
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FT	Region	53. .59
FT		/label= CDR2
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FT	Misc-difference	207
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PF	27-SEP-2000; 2000WO-US026619.	
XX		
PR	27-SEP-1999; 99US-0156194P.	
PR	31-MAY-2000; 2000US-0208684P.	
XX		
PA	(REGC ) UNIV CALIFORNIA.	
XX		
PI	Meares C, Chmura A;	
XX		
DR	WPI; 2001-244971/25.	
DR	N-PSDB; AAF30635.	
XX		
PT	Nucleic acid encoding a mutant antibody comprising a reactive site that	
PT	specifically binds to a metal chelate useful as analytical agents and in	
PT	clinical diagnosis, as well as in the treatment of disease, particularly	
PT	cancer.	
XX		
PS	Disclosure; Fig 14; 100pp; English.	

XX

CC The invention provides a mutant antibody comprising a reactive site that  
CC is not present in the wild-type of the antibody. The antibody also has a  
CC complementarity determining region (CDR) that specifically binds to a  
CC metal chelate against which the wild-type antibody is raised. The  
CC reactive site of the mutant antibody is in a position proximate to or  
CC within the CDR, such that the chelate and the antibody are able to form a  
CC covalent bond. The present sequence is that of the light chain variable  
CC region of anti-indium-EDTA monoclonal antibody CHA255, carrying a S95C  
CC mutation. As an example of the method of the invention, rational computer  
CC -aided design was used to develop an indium-EDTA chelate to covalently  
CC bind to CHA255 in vivo. The premise was to allow the chelate to bind non-  
CC covalently to CHA255 bound to a tumour and then to covalently attach the  
CC chelate to the antibody, thereby trapping it at the tumour site. This  
CC involved cloning the variable domains of CHA255 to construct a  
CC human/mouse chimeric Fab fragment that could be expressed in Escherichia  
CC coli, and the synthesis and screening of benzyl-EDTA chelates carrying  
CC weakly electrophilic groups capable of conjugation of the antibody in  
CC vivo. This Fab can be conjugated to a targeting moiety when desired. A  
CC reactive site was incorporated into the antibody by engineering a Cys  
CC residue at location Asn-96 or Ser-95 of the light chain, near the region  
CC of the antibody to which the chelate bound. This was accomplished by site  
CC -directed mutagenesis of a nucleic acid encoding the wild-type of the  
CC anti-chelate antibody

XX

SQ Sequence 218 AA;

Query Match 99.8%; Score 1132; DB 4; Length 218;  
Best Local Similarity 100.0%; Pred. No. 3.9e-79;  
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60  
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Db 1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60  
  
Qy 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120  
|  
Db 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120  
  
Qy 121 IFPPSDEQLKSGTASVVCLLNNFYFPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180  
|  
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Qy 181 STLTLKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218  
|  
Db 181 STLTLKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218

us-09-671-953b-7.ra1

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2005, 15:23:21 ; Search time 30 seconds  
(without alignments)  
542.450 Million cell updates/sec

Title: US-09-671-953B-7  
Perfect score: 1134  
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	757	66.8	235	3	US-09-423-439-18	Sequence 18, Appl
2	750	66.1	220	3	US-08-952-235-1	Sequence 1, Appli
3	750	66.1	220	4	US-09-669-971-1	Sequence 1, Appli
4	743	65.5	233	4	US-09-472-087-15	Sequence 15, Appl
5	743	65.5	233	4	US-09-472-087-67	Sequence 67, Appl
6	739	65.2	213	3	US-08-397-411-12	Sequence 12, Appl
7	736	64.9	235	4	US-09-011-769A-27	Sequence 27, Appl
8	734	64.7	236	4	US-09-315-926A-79	Sequence 79, Appl
9	732.5	64.6	234	4	US-09-472-087-17	Sequence 17, Appl
10	732.5	64.6	234	4	US-09-472-087-69	Sequence 69, Appl
11	732	64.6	235	4	US-09-472-087-14	Sequence 14, Appl
12	732	64.6	235	4	US-09-472-087-65	Sequence 65, Appl
13	731.5	64.5	224	4	US-09-456-090A-84	Sequence 84, Appl
14	731.5	64.5	224	4	US-09-453-234-84	Sequence 84, Appl
15	730.5	64.4	491	4	US-10-011-125A-2	Sequence 2, Appli
16	728.5	64.2	214	3	US-08-397-411-5	Sequence 5, Appli
17	728	64.2	239	4	US-09-627-896B-22	Sequence 22, Appl



					us-09-671-953b-7.rai	
18	726.5	64.1	214	4	US-09-472-087-71	Sequence 71, Appl
19	726.5	64.1	224	4	US-09-456-090A-46	Sequence 46, Appl
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21	725	63.9	234	4	US-09-740-002-26	Sequence 26, Appl
22	724.5	63.9	234	4	US-09-740-002-24	Sequence 24, Appl
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24	724	63.8	235	3	US-09-171-945-17	Sequence 17, Appl
25	722.5	63.7	224	4	US-09-456-090A-36	Sequence 36, Appl
26	722.5	63.7	224	4	US-09-453-234-36	Sequence 36, Appl
27	722.5	63.7	226	4	US-09-456-090A-74	Sequence 74, Appl
28	722.5	63.7	226	4	US-09-453-234-74	Sequence 74, Appl
29	722	63.7	233	3	US-09-485-737B-69	Sequence 69, Appl
30	722	63.7	233	4	US-10-071-485-69	Sequence 69, Appl
31	721.5	63.6	218	5	PCT-US96-13152-2	Sequence 2, Appli
32	721.5	63.6	236	1	US-08-157-101A-5	Sequence 5, Appli
33	720.5	63.5	213	3	US-08-630-820-6	Sequence 6, Appli
34	720.5	63.5	213	4	US-09-273-453-6	Sequence 6, Appli
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37	719	63.4	219	4	US-09-121-952A-72	Sequence 72, Appl
38	719	63.4	219	4	US-09-234-340A-72	Sequence 72, Appl
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41	719	63.4	242	3	US-08-804-444A-56	Sequence 56, Appl
42	719	63.4	242	3	US-09-026-985-56	Sequence 56, Appl
43	719	63.4	242	4	US-09-121-952A-56	Sequence 56, Appl
44	719	63.4	242	4	US-09-234-340A-56	Sequence 56, Appl
45	718.5	63.4	214	3	US-09-247-352-4	Sequence 4, Appli

# ALIGNMENTS

## RESULT 1

US-09-423-439-18

; Sequence 18, Application US/09423439

; Patent No. 6339070

### GENERAL INFORMATION:

APPLICANT: EMERY, Stephen Charles

BLAKEY, David Charles

TITLE OF INVENTION: CHEMICAL COMPOUNDS

NUMBER OF SEQUENCES: 60

### CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Winthrop, L.L.P.

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

### COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS word

### CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/423,439

FILING DATE: 09-No. 6339070-1999

CLASSIFICATION: <Unknown>

### PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB98/01294

FILING DATE: 05-MAY-1998

APPLICATION NUMBER: GB 9709421.3

FILING DATE: 10-MAY-1997

us-09-671-953b-7.ra

; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-423-439-18

Query Match 66.8%; Score 757; DB 3; Length 235;
Best Local Similarity 71.8%; Pred. No. 7.9e-67;
Matches 155; Conservative 15; Mismatches 40; Indels 6; Gaps 3;

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Db 200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235

us-09-671-953b-7.rapb

GenCore version 5.1.6  
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802.937 Million cell updates/sec

Title: US-09-671-953B-7  
Perfect score: 1134  
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

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Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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us-09-671-953b-7.rapb						
2	1083	95.5	218	17	US-10-631-258-27	Sequence 27, Appl
3	1083	95.5	218	18	US-10-350-555-27	Sequence 27, Appl
4	1082	95.4	218	16	US-10-625-047-28	Sequence 28, Appl
5	1082	95.4	218	17	US-10-631-258-28	Sequence 28, Appl
6	1082	95.4	218	18	US-10-350-555-28	Sequence 28, Appl
7	759.5	67.0	235	16	US-10-723-003-42	Sequence 42, Appl
8	759.5	67.0	235	20	US-11-004-639-42	Sequence 42, Appl
9	759	66.9	213	17	US-10-822-231-3	Sequence 3, Appli
10	759	66.9	213	18	US-10-880-028-49	Sequence 49, Appl
11	759	66.9	213	18	US-10-880-320-49	Sequence 49, Appl
12	754.5	66.5	235	20	US-11-019-180-2	Sequence 2, Appli
13	753	66.4	213	14	US-10-150-475A-8	Sequence 8, Appli
14	753	66.4	213	16	US-10-704-522-8	Sequence 8, Appli
15	753	66.4	213	16	US-10-645-215-8	Sequence 8, Appli
16	753	66.4	213	20	US-11-136-538-9	Sequence 9, Appli
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20	751	66.2	213	20	US-11-136-538-8	Sequence 8, Appli
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22	750	66.1	220	14	US-10-232-408-1	Sequence 1, Appli
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24	746	65.8	215	18	US-10-830-956-32	Sequence 32, Appl
25	745	65.7	213	15	US-10-435-299-12	Sequence 12, Appl
26	745	65.7	213	17	US-10-822-300-135	Sequence 135, App
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41	739.5	65.2	234	15	US-10-045-674-587	Sequence 587, App
42	739	65.2	215	15	US-10-307-724-122	Sequence 122, App
43	739	65.2	215	16	US-10-737-290-122	Sequence 122, App
44	739	65.2	239	16	US-10-737-290-142	Sequence 142, App
45	738	65.1	213	15	US-10-474-832-3	Sequence 3, Appli

#### ALIGNMENTS

RESULT 1  
 US-10-625-047-27  
 ; Sequence 27, Application US/10625047  
 ; Publication No. US20040198962A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Meares, Claude  
 ; APPLICANT: Corneillie, Todd  
 ; APPLICANT: The Regents of the University of California  
 ; TITLE OF INVENTION: Multi-Functional Antibodies  
 ; FILE REFERENCE: 023070-130910US  
 ; CURRENT APPLICATION NUMBER: US/10/625,047  
 ; CURRENT FILING DATE: 2003-07-22  
 ; PRIOR APPLICATION NUMBER: US 10/350,555  
 ; PRIOR FILING DATE: 2003-01-23

us-09-671-953b-7.rapb

; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:native cloned  
; OTHER INFORMATION: chimeric murine 2D12.5 light chain variable region  
; OTHER INFORMATION: (VL) fused to human anti-tetanus toxin antibody  
; OTHER INFORMATION: kappa light chain constant region (TTCL)  
US-10-625-047-27

Query Match 95.5%; Score 1083; DB 16; Length 218;  
Best Local Similarity 95.9%; Pred. No. 1.2e-84;  
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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## RESULT 2

US-10-631-258-27

; Sequence 27, Application US/10631258  
; Publication No. US20050026263A1  
; GENERAL INFORMATION:  
; APPLICANT: Meares, Claude  
; APPLICANT: Corneillie, Todd  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Multi-Functional Antibodies  
; FILE REFERENCE: 023070-130920US  
; CURRENT APPLICATION NUMBER: US/10/631,258  
; CURRENT FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: US 10/350,555  
; PRIOR FILING DATE: 2003-01-23  
; PRIOR APPLICATION NUMBER: US 10/625,047  
; PRIOR FILING DATE: 2003-07-22  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:native cloned  
; OTHER INFORMATION: chimeric murine 2D12.5 light chain variable region  
; OTHER INFORMATION: (VL) fused to human anti-tetanus toxin antibody  
; OTHER INFORMATION: kappa light chain constant region (TTCL)  
US-10-631-258-27

us-09-671-953b-7.rapb  
Query Match 95.5%; Score 1083; DB 17; Length 218;  
Best Local Similarity 95.9%; Pred. No. 1.2e-84;  
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db    121 IFPPSDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDYSTYSL 180

Qy    181 STLTLKADYKHKVYACEVTHQGLSPVTKSFNRGEC 218
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Db    181 STLTLKADYKHKVYACEVTHQGLSPVTKSFNRGEC 218

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# RESULT 3

US-10-350-555-27

; Sequence 27, Application US/10350555

; Publication No. US20040146934A1

## GENERAL INFORMATION:

; APPLICANT: Meares, Claude

; APPLICANT: Corneillie, Todd

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Multi-Functional Antibodies

; FILE REFERENCE: 023070-130900US

; CURRENT APPLICATION NUMBER: US/10/350,555

; CURRENT FILING DATE: 2003-01-23

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 27

; LENGTH: 218

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:native cloned

; OTHER INFORMATION: chimeric murine 2D12.5 light chain variable region

; OTHER INFORMATION: (VL) fused to human anti-tetanus toxin antibody

; OTHER INFORMATION: kappa light chain constant region (TTCL)

US-10-350-555-27

Query Match 95.5%; Score 1083; DB 18; Length 218;  
Best Local Similarity 95.9%; Pred. No. 1.2e-84;  
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy      1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60
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Qy    121 IFPPSDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDYSTYSL 180
      |||
Db    121 IFPPSDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDYSTYSL 180

Qy    181 STLTLKADYKHKVYACEVTHQGLSPVTKSFNRGEC 218

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us-09-671-953b-7.rapb

Db

|||||  
181 STLTLKADYEKHKVYACEVTHQGLSLPVTKSFNREGC 218

RESULT 4

US-10-625-047-28

; Sequence 28, Application US/10625047  
; Publication No. US20040198962A1  
; GENERAL INFORMATION:  
; APPLICANT: Meares, Claude  
; APPLICANT: Corneillie, Todd  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Multi-Functional Antibodies  
; FILE REFERENCE: 023070-130910US  
; CURRENT APPLICATION NUMBER: US/10/625,047  
; CURRENT FILING DATE: 2003-07-22  
; PRIOR APPLICATION NUMBER: US 10/350,555  
; PRIOR FILING DATE: 2003-01-23  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:N53C cloned  
; OTHER INFORMATION: mutant chimeric murine 2D12.5 light chain variable  
; OTHER INFORMATION: region (VL) fused to human anti-tetanus toxin  
; OTHER INFORMATION: antibody kappa light chain constant region (TTCL)  
US-10-625-047-28

Query Match 95.4%; Score 1082; DB 16; Length 218;  
Best Local Similarity 95.9%; Pred. No. 1.5e-84;  
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60  
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Db 1 RSAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGCNNRPPG 60  
  
Qy 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120  
|||  
Db 61 VPARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTKLTVLSRTVAAPSVF 120  
  
Qy 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180  
|||  
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180  
  
Qy 181 STLTLKADYEKHKVYACEVTHQGLSXPVTKSFNREGC 218  
|||  
Db 181 STLTLKADYEKHKVYACEVTHQGLSLPVTKSFNREGC 218

RESULT 5

US-10-631-258-28

; Sequence 28, Application US/10631258  
; Publication No. US20050026263A1  
; GENERAL INFORMATION:  
; APPLICANT: Meares, Claude  
; APPLICANT: Corneillie, Todd  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Multi-Functional Antibodies  
; FILE REFERENCE: 023070-130920US  
; CURRENT APPLICATION NUMBER: US/10/631,258

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                                us-09-671-953b-7.rapb
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US 10/350,555
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: US 10/625,047
; PRIOR FILING DATE: 2003-07-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 218
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:N53C cloned
;   OTHER INFORMATION: mutant chimeric murine 2D12.5 light chain variable
;   OTHER INFORMATION: region (VL) fused to human anti-tetanus toxin
;   OTHER INFORMATION: antibody kappa light chain constant region (TTCL)
US-10-631-258-28

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Query Match          95.4%; Score 1082; DB 17; Length 218;
Best Local Similarity 95.9%; Pred. No. 1.5e-84;
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy      1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60
        |||
Db      1 RSAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGCNNRPPG 60
        |||
Qy      61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120
        |||
Db      61 VPARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTKLTVLSRTVAAPSVF 120
        |||
Qy      121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYSL 180
        |||
Db      121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYSL 180
        |||
Qy      181 STLTLKADYEEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
        |||
Db      181 STLTLKADYEEKHKVYACEVTHQGLSLPVTKSFNRGEC 218
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RESULT 6
US-10-350-555-28
; Sequence 28, Application US/10350555
; Publication No. US20040146934A1
; GENERAL INFORMATION:
;   APPLICANT: Meares, Claude
;   APPLICANT: Corneillie, Todd
;   APPLICANT: The Regents of the University of California
;   TITLE OF INVENTION: Multi-Functional Antibodies
;   FILE REFERENCE: 023070-130900US
;   CURRENT APPLICATION NUMBER: US/10/350,555
;   CURRENT FILING DATE: 2003-01-23
;   NUMBER OF SEQ ID NOS: 72
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 218
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:N53C cloned
;   OTHER INFORMATION: mutant chimeric murine 2D12.5 light chain variable
;   OTHER INFORMATION: region (VL) fused to human anti-tetanus toxin
;   OTHER INFORMATION: antibody kappa light chain constant region (TTCL)
US-10-350-555-28

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us-09-671-953b-7.rapb

Query Match 95.4%; Score 1082; DB 18; Length 218;  
Best Local Similarity 95.9%; Pred. No. 1.5e-84;  
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy	1	RSAVVTQESALTTSPGETVTLTCSRSSIGAVTTSNYANWVQEKPDLHFTGLIGGTNNRAPG	60
Db	1	RSAVVTQESALTTSPGETVTLTCSRSTGAVTTSNYANWVQEKPDLHFTGLIGGCNRRPPG	60
Qy	61	VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWFVGGGTKLTVLSRTVAAPSVF	120
Db	61	VPARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWFVGGGTKLTVLSRTVAAPSVF	120
Qy	121	IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS	180
Db	121	IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS	180
Qy	181	STLTLSKADYEKKHKVYACEVTHQGLSXPVTKSFNRGEC	218
Db	181	STLTLSKADYEKKHKVYACEVTHQGLSLPVTKSFNREGC	218

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2005, 15:22:51 ; Search time 25.5 Seconds  
(without alignments)  
822.559 Million cell updates/sec

Title: US-09-671-953B-7  
Perfect score: 1134  
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pirl:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	739	65.2	215	2	JE0242	Ig kappa chain NIG
2	735	64.8	215	2	JE0244	Ig kappa chain NIG
3	728.5	64.2	214	2	PC4156	Ig lambda chain V
4	721	63.6	215	2	JE0243	Ig kappa chain NIG
5	678.5	59.8	216	2	JE0241	Ig kappa chain Am3
6	672	59.3	215	2	A23746	Ig kappa chain V-I
7	578.5	51.0	135	2	S52059	JC-kappa protein -
8	549.5	48.5	240	2	S06084	Ig kappa chain pre
9	547.5	48.3	287	4	PC4402	pelB leader/Ig hea
10	544	48.0	106	1	K3HU	Ig kappa chain C r
11	541	47.7	128	2	S52450	Ig lambda chain V
12	534.5	47.1	220	2	A31790	Ig kappa chain V r
13	533	47.0	129	1	L1MS4E	Ig lambda-1 chain

14	526	46.4	235	2	S25058	Ig kappa chain - m
15	525	46.3	113	2	S06819	Ig lambda chain V
16	523.5	46.2	112	2	S06818	Ig lambda chain V
17	521	45.9	106	2	S20654	Ig lambda chain V
18	513.5	45.3	114	2	S06820	Ig lambda chain V
19	511	45.1	219	2	S38865	Ig kappa chain - m
20	511	45.1	225	2	S37484	Ig kappa chain - m
21	509	44.9	99	2	A37927	Ig kappa chain C r
22	504.5	44.5	234	2	S14237	Ig kappa chain pre
23	503	44.4	99	2	S26653	Ig kappa chain C r
24	502.5	44.3	230	2	S33161	Ig kappa chain - s
25	500	44.1	113	2	B54256	Ig lambda-1 chain
26	499.5	44.0	114	2	S06822	Ig lambda chain V
27	498	43.9	129	1	L2MS35	Ig lambda-2 chain
28	497.5	43.9	214	2	S68212	Ig kappa chain (Ma
29	497.5	43.9	218	2	S68241	Ig kappa chain V r
30	495.5	43.7	225	2	JL0029	Ig kappa chain pre
31	495.5	43.7	234	2	S01320	Ig kappa chain pre
32	492.5	43.4	218	2	JC5810	monoclonal antibod
33	490	43.2	217	2	S42772	Ig kappa chain - m
34	488.5	43.1	99	2	PH1089	Ig lambda chain V
35	488	43.0	219	2	S16112	Ig kappa chain V r
36	486	42.9	99	2	S14582	Ig lambda chain V
37	486	42.9	113	2	S06821	Ig lambda chain V
38	485	42.8	235	2	S25749	Ig lambda chain -
39	484.5	42.7	219	2	PC4203	Ig kappa chain (mo
40	478	42.2	97	2	PH1090	Ig lambda chain V
41	478	42.2	116	1	L1MSV	Ig lambda-1 chain
42	478	42.2	219	2	S52028	Ig kappa chain - m
43	473	41.7	99	2	S14584	Ig lambda chain V
44	473	41.7	100	2	PH1088	Ig lambda chain V
45	469.5	41.4	210	2	A56169	Ig kappa chain V r

#### ALIGNMENTS

##### RESULT 1

JE0242

Ig kappa chain NIG26 precursor - human

C;Species: Homo sapiens (man)

C;Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

C;Accession: JE0242

R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.

submitted to JIPID, November 1998

A;Description: Structure relationship of kappatype light chains with AL amyloidosis: Multiple deletions found in a VkIV protein.

A;Reference number: JE0241

A;Accession: JE0242

A;Molecule type: protein

A;Residues: 1-215 <ALI>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 65.2%; Score 739; DB 2; Length 215;  
Best Local Similarity 70.4%; Pred. No. 1.4e-48;

Matches 152; Conservative 17; Mismatches 43; Indels 4; Gaps 3;

Qy 4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62  
|:| | : | | | | | : | | | | : | | : | | | : |

Db 3 VLTQSPGTLSSLSPGERATLSCRAS--QSVSNNYLAWYQQKPGQAPSLLIYDASSRATGIP 60

Qy 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122  
| | | | | | | | | | : | | | | : | | | | : | | | | | | | | | | | |

Db 61 DRFSGSGSGTDFILTISGLEPEDFAVYYCQYDRPPWTFGQGTKVEI-KRTVAAPSVFIF 119

Qy 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSS 182  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSS 179

Qy 183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 180 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215

us-09-671-953b-7.rup

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2005, 15:22:03 ; Search time 116.5 Seconds  
(without alignments)  
958.225 Million cell updates/sec

Title: US-09-671-953B-7  
Perfect score: 1134  
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries.

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	732	64.6	235	2	Q6GMW0	Q6gmw0 homo sapien
2	731	64.5	235	2	Q6PJF2	Q6pjf2 homo sapien
3	728	64.2	236	2	Q6GMW1	Q6gmw1 homo sapien
4	725	63.9	234	2	Q7Z473	Q7z473 homo sapien
5	722.5	63.7	236	2	Q7Z3Y4	Q7z3y4 homo sapien
6	721	63.6	235	2	Q6GMV9	Q6gmv9 homo sapien
7	720.5	63.5	236	2	Q6GMX9	Q6gmx9 homo sapien
8	720.5	63.5	236	2	Q6PIH7	Q6pih7 homo sapien
9	719.5	63.4	236	2	Q6P5S8	Q6p5s8 homo sapien
10	717.5	63.3	236	2	Q6PIL8	Q6pil8 homo sapien
11	714.5	63.0	236	2	Q6GMX0	Q6gmx0 homo sapien
12	709.5	62.6	236	2	Q6GMX8	Q6gmx8 homo sapien
13	706.5	62.3	236	2	Q6PIH4	Q6pih4 homo sapien
14	699	61.6	236	2	Q6PIT5	Q6pit5 homo sapien
15	695	61.3	240	2	Q6PIH6	Q6pih6 homo sapien
16	692	61.0	239	2	Q8NEK0	Q8nek0 homo sapien
17	692	61.0	239	2	Q8TCD0	Q8tcd0 homo sapien
18	663	58.5	239	2	Q6P491	Q6p491 homo sapien
19	564.5	49.8	120	2	Q6P5R5	Q6p5r5 homo sapien
20	544	48.0	106	1	KAC_HUMAN	P01834 homo sapien
21	539	47.5	129	1	LV1E_MOUSE	P01727 mus musculus

				us-09-671-953b-7.rup				
22	534	47.1	129	1	LV1D_MOUSE	P01726	mus	musculu
23	533	47.0	129	1	LV1B_MOUSE	P01724	mus	musculu
24	527	46.5	129	2	Q8VDE2	Q8vde2	mus	musculu
25	525	46.3	110	1	LV1C_MOUSE	P01725	mus	musculu
26	518.5	45.7	113	2	Q8CGS1	Q8cgs1	mus	musculu
27	516.5	45.5	238	2	Q66JS7	Q66js7	mus	musculu
28	512.5	45.2	109	2	Q9ET13	Q9et13	mus	musculu
29	505.5	44.6	236	2	Q7TS98	Q7ts98	mus	musculu
30	498	43.9	129	1	LV2B_MOUSE	P01729	mus	musculu
31	498	43.9	219	2	Q65ZC0	Q65zc0	mus	musculu
32	493.5	43.5	241	2	Q63ZX4	Q63zx4	mus	musculu
33	478	42.2	117	1	LV1A_MOUSE	P01723	mus	musculu
34	450	39.7	117	1	LV2A_MOUSE	P01728	mus	musculu
35	441.5	38.9	236	2	Q8NEJ1	Q8nej1	homo	sapien
36	440	38.8	235	2	Q6IN99	Q6in99	homo	sapien
37	434	38.3	248	2	Q7SYU1	Q7syu1	xenopus	lae
38	432.5	38.1	236	2	Q6IPQ0	Q6ipq0	homo	sapien
39	430.5	38.0	236	2	Q6PIQ7	Q6piq7	homo	sapien
40	430	37.9	233	2	Q8TBC9	Q8tbc9	homo	sapien
41	428.5	37.8	230	2	Q7Z2U3	Q7z2u3	homo	sapien
42	427.5	37.7	236	2	Q6GMV7	Q6gmv7	homo	sapien
43	425.5	37.5	234	2	Q7Z2U7	Q7z2u7	homo	sapien
44	424	37.4	231	2	Q6GNB8	Q6gnb8	xenopus	lae
45	424	37.4	233	2	Q8N5F4	Q8n5f4	homo	sapien

#### ALIGNMENTS

#### RESULT 1

Q6GMW0

ID Q6GMW0 PRELIMINARY; PRT; 235 AA.  
AC Q6GMW0;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human

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us-09-671-953b-7.rup
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC073792; AAH73792.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

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Query Match 64.6%; Score 732; DB 2; Length 235;  
Best Local Similarity 70.3%; Pred. No. 5e-56;  
Matches 154; Conservative 16; Mismatches 39; Indels 10; Gaps 5;

Best Local Similarity 70.3%; Pred. No. 5e-56;

Matches 154; Conservative 16; Mismatches 39; Indels 10; Gaps 5;

Qy 4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDLHFTGLIGGTNNRAPGVP 62  
| : | | | : | | | | | : | : | : | : | : | : | : |  
Db 23 VMTQSPATLSVSPGERATLSCRAS---QSISNNLAWYQQRPGQAPRLLIYGASSRVTGIP 79

Qy 63 ARFSGSLIGDKAALTITGAQTEDEARYFCAL---WYCNLWVFGGGTKLTVLSRTVAAPSV 119  
| | | | | : | : | : | : | | | | | : | | | | : | | | | |  
Db 80 GRFSGSGSGTEFTLSISSLQSEDFAVYFCQQYNWL--LYTFQGGTKLEI-KRTVAAPSV 136

Qy 120 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSYL 179  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 137 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSYL 196

Qy 180 SSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 197 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235

Db 23 VMTQSPATLSVSPGERATLSCRAS---QSIENNLAWYQORPGOAPRLLIYGASSRVTGIP 79

QY 63 ARFSGSLIGDKAALITITGAQTEDEARYFCAL---WYCNLWVFGGGTKLTVLSRTVAAPSV 119

Db 80 GRFSGSGSGTEFTLSISLQSEDAVYFCQQYNDWL--LYTFGQGTKLEI-KRTVAAPSV 136

Qy 120 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179

Db 137 FIFPPSDEQLKSGTASVCLLNFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSYL 196

Qy 180 SSTLTLSKADYEKHKVYACEVTHQGLSXPTKSFNRGEC 218

db 197 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235